

Figure 1

1	GATTCGGCAGAGAACTTTTAAATCTTTAGTTATTTCTTAATACTTAGAACACTTAAAC	60
61	AAAACTTTACAAAACAAAAGAGCAGAATAATTAGATCCTTTCAGGAGAATATGACTTTTT	120
121	TTTCCTAAGCACACTGGACCATAGAGGAAGACCAAAGGAATGTACAGTTGCCTGCTCCTT	180
1	M Y S C L L L	7
181	CCTGACTTGCTGTATTTgACTCTGtCCCCACTGGTGGTGGCAATGCTATTAACCCACAC	240
8	P D L L Y L T L S P L V V A M L L T P H	27
241	TTTAACGTGGCAAATCCCCAGAATCTGTTGGCTGGTCTCTGGCTAGAGAATGAGCACAGT	300
28	F N V A N P Q N L L A G L W L E N E H S	47
301	TTCACCCTTATGGCTCCAGAAAGAGCAAGAACACACCACTGCCAGCCAGAAGAGAGAAAA	360
48	F T L M A P E R A R T H H C Q P E E R K	67
361	GTCTTGTTCTGTCTCTTTCCCATGTCCCAAATAGCCAAGCACAGGTTCAACCACCCCAA	420
68	V L F C L F P I V P N S Q A Q V Q P P Q	87
421	ATGCCACCCTTCTGCTGTGCAGCAGCCAAGGAAAAGACCCAGGAGGAGCAGCTCCAAGAA	480
88	M P P F C C A A A K E K T Q E E Q L Q E	107
481	CCTCTGGGCAGTCAGTGCCAGATACTTGCCCCAATTCTTTGTGTCCAAGCCACACTCAG	540
108	P L G S Q C P D T C P N S L C P S H T Q	127
541	CTGACAAAAGCCAACACTTTGTCTCTCTTTTTTTTTTTTTCTTTTTTTTTTGAGCAGAGTT	600
128	L T K A N T L S L F F F F S F F L S R V	147
601	TCACTCTTGTCACCCAGGCTGGAGTGCAATgCAGGATCTTGGCTCATTGCAACCTCCAC	660
148	S L L S P R L E C N G R I L A H C N L H	167
661	CtCCCCGGGTTCAAGCAATTCTCCTGTCTCAGCCTCTCGA	699
168	L P G S S N S P V S A S R	180

Figure 2

